BISS Biodiversity Information Science and Standards

Biodiversity Information Science and Standards 9: e175153
doi: 10.3897/biss.9.175153

OPEN ACCESS

Conference Abstract

The Swedish Reference Genome Portal: A Hub for Non-Human Eukaryotic Genomic Data Visualisation, Discovery, and Reuse

Henrik Lantz‡, Daniel Brink§, Rory Crean§, Quentin Ågren|, Hanna Kultima§, Bengt Persson‡, Johan Rung§, Angela P. Fuentes-Pardo§

‡ National Bioinformatics Infrastructure Sweden, Science for Life Laboratory, Uppsala University, Uppsala, Sweden
§ Science for Life Laboratory Data Centre, Uppsala University, Uppsala, Sweden
| Science for Life Laboratory Data Centre, Swedish Museum of Natural History, Stockholm, Sweden

Corresponding author: Henrik Lantz (henrik.lantz@scilifelab.se),
Angela P. Fuentes-Pardo (apfpgen@gmail.com)

Received: 16 Oct 2025 | Published: 24 Nov 2025

Citation: Lantz H, Brink D, Crean R, Ågren Q, Kultima H, Persson B, Rung J, Fuentes-Pardo AP (2025) The Swedish Reference Genome Portal: A Hub for Non-Human Eukaryotic Genomic Data Visualisation, Discovery, and Reuse. Biodiversity Information Science and Standards 9: e175153. https://doi.org/10.3897/biss.9.175153

Abstract

Non-human eukaryotic genome assemblies and annotations are frequently dispersed across repositories, supplementary materials, or remain unpublished. Their access often requires technical expertise and large downloads, hindering usability. The Swedish Reference Genome Portal*[1] (SRGP) offers a web platform to easily find, explore, and share genomic data from non-human eukaryotic species studied in Sweden.

The SRGP gathers assemblies and annotations into species-specific pages with an interactive JBrowse2 genome browser, metadata, and download links (Fig. 1). This web interface provides user-friendly visualisations aimed at broad user communities, particularly in biodiversity and evolution.

Unlike global resources such as Ensembl or the UCSC Genome Browser, which focus on model organisms, the SRGP showcases species studied in Swedish institutions. It fosters community-driven data sharing and broadens access to genomic annotations that are rarely published (e.g., from population genomics), while adhering to Findable,

© Lantz H et al. This is an open access article distributed under the terms of the Creative Commons Attribution License (CC BY 4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Accessible, Interoperable and Reusable (FAIR) principles. In doing so, it bridges global infrastructures with local research needs, enabling both specialists and non-specialists to make better use of genomic data.

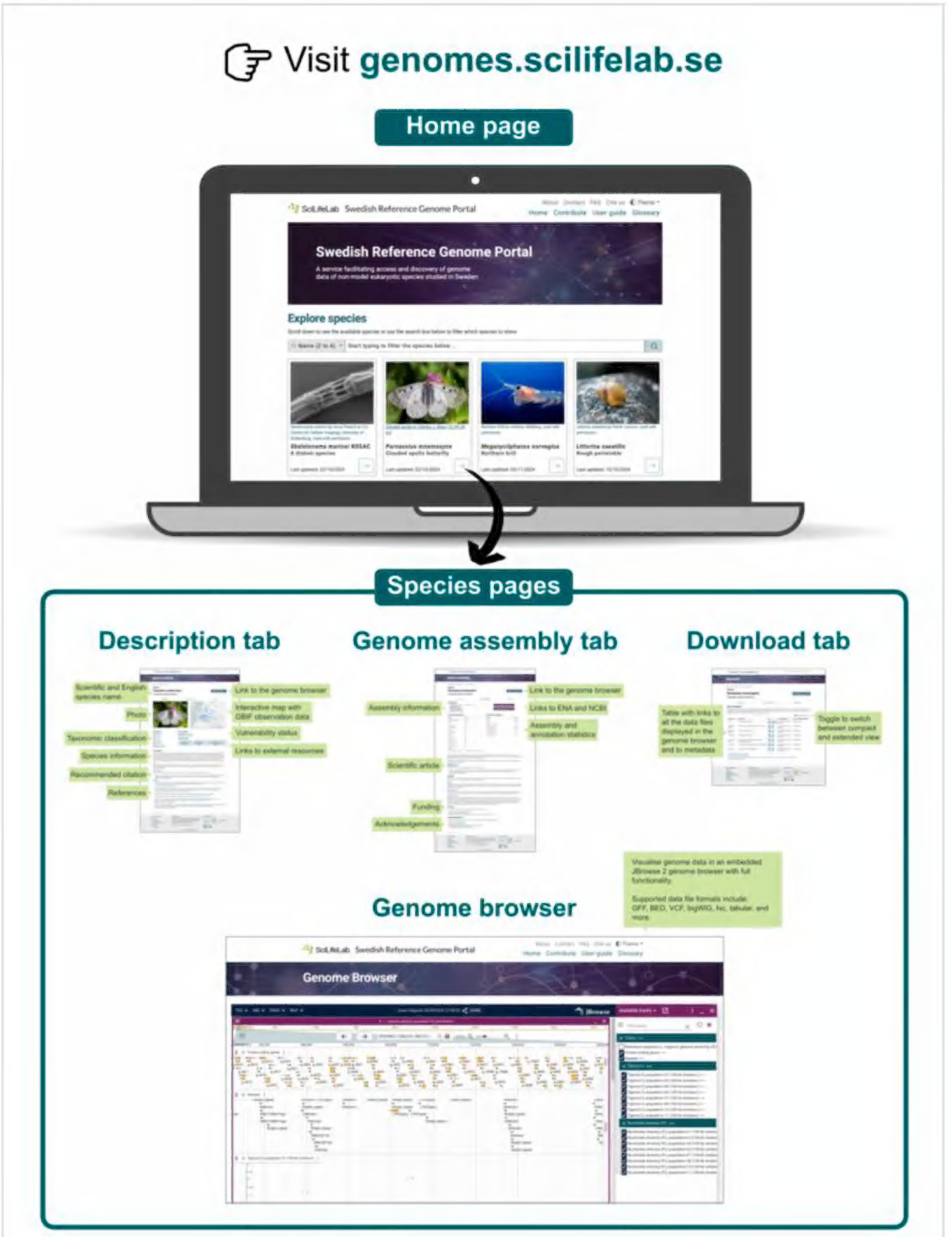

Figure 1.

Home page and species pages of the Swedish Reference Genome Portal.

The technical architecture of the SRGP (Fig. 2) is designed to make the service easy to use and reuse by others:

- **Simple and secure**: Built with Hugo, a static site generator that requires no databases or heavy servers, enabling lightweight maintenance.
- **Lightweight and fast**: Composed of prebuilt pages and files for quick loading and easy scalability.
- **Open and reusable**: Fully open-source, allowing others to adapt and extend the code.
- **Easy to update**: New species or datasets can be added by editing configuration files and rebuilding the site.
- **Portable**: Packaged with Docker for easy deployment anywhere, including Kubernetes clusters.
- **User-friendly**: Integrates JBrowse2 for interactive exploration of genomic data.

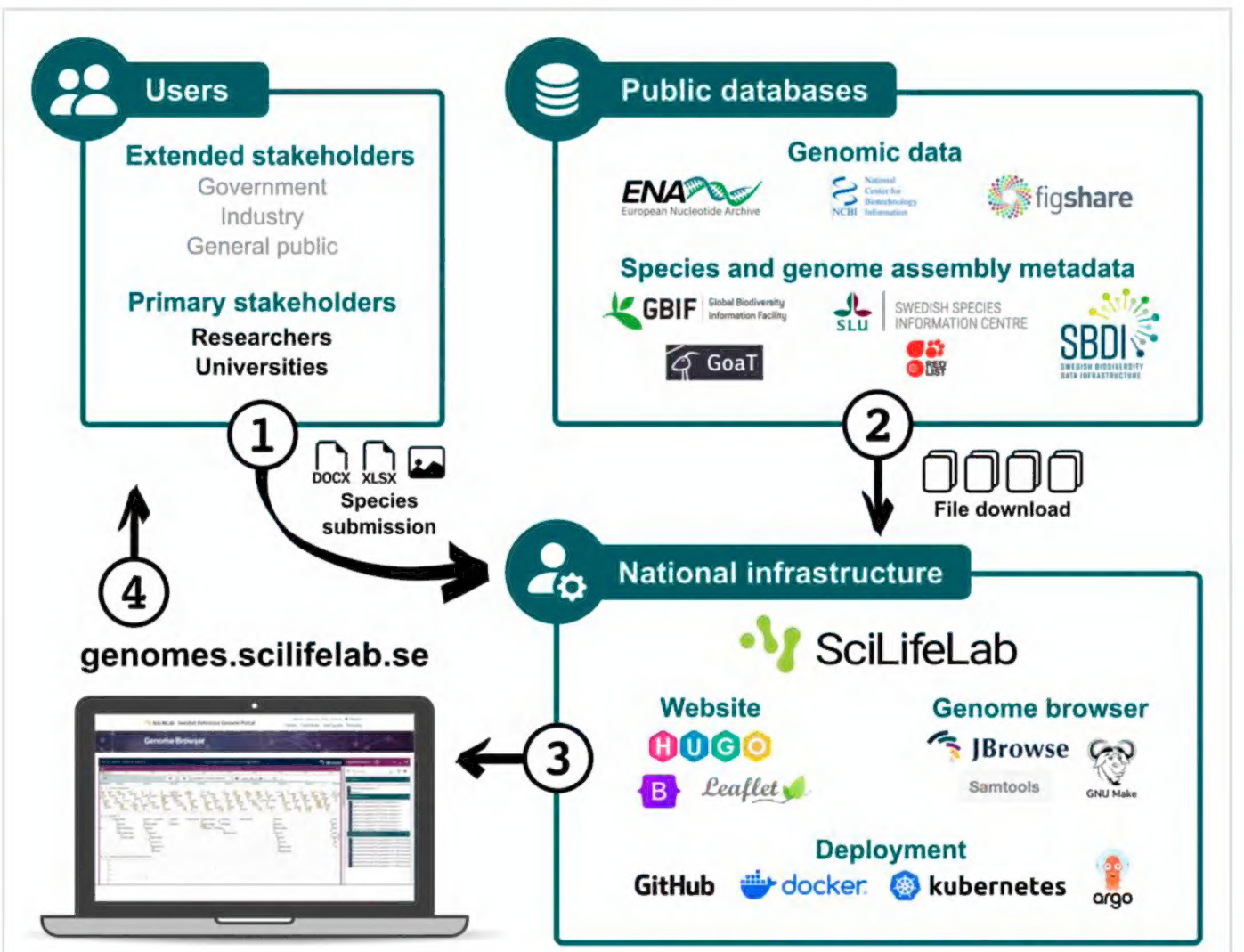

Figure 2.

Swedish Reference Genome Portal architecture and data flow, by SciLifeLab Data Centre (2025), license CC BY 4.0.

1. Users submit species information, data tracks, and an image to SciLifeLab.
2. Data are fetched from public repositories.
3. Species pages are created, and data are integrated into the genome browser.
4. Webpages are openly accessible online.

The SRGP is designed for simple deployment and maintenance. Genome data and annotations are processed with automated scripts in Docker containers to ensure consistency and reproducibility. The website is built with Hugo, which generates fast, lightweight pages requiring no database. Both data and pages are bundled into Docker images and deployed on a Kubernetes cluster, with ArgoCD handling updates automatically. This setup provides reliable operation on standard infrastructure, easy scaling for new datasets, and secure, low-maintenance access to genomic resources (Fig. 2).

In summary, the SRGP makes previously hidden genomic data, especially from local or specialised communities, easy to find and explore through a single, user-friendly browser. It lowers access barriers while remaining simple, fast, and scalable. By unifying scattered resources, it provides a reusable model for other countries, institutions, or research groups. This presentation is available in (presentación disponible en español en) Fuentes-Pardo et al. (2025).

Keywords

assembly, genome browser, genomic annotation, JBrowse2, open source, open science, data visualisation

Presenting author

Angela P. Fuentes-Pardo

Presented at

Living Data 2025

Acknowledgements

This work is developed and operated by Science for Life Laboratory (SciLifeLab) Data Centre, with support from the SciLifeLab & Wallenberg National Program for Data-Driven Life Science and the Swedish Foundation for Strategic Research (SSF). The SciLifeLab Data Centre extends its gratitude to national and international repositories, including the European Nucleotide Archive (ENA), National Center for Biotechnology Information (NCBI), SciLifeLab Data Repository, Swedish Biodiversity Data Infrastructure, SLU Swedish Species Information Centre, Genomes on a Tree (GoaT), Global Biodiversity Information Facility (GBIF), and IUCN Red List of Threatened Species, from which it retrieves data. These resources enable researchers and the wider community to access valuable information openly. We are also grateful for the open-source software that was crucial for the development of this web platform, including Hugo, Bootstrap, Leaflet, JBrowse2, SAMtools, GNU Make, and Kubernetes.

Conflicts of interest

The authors have declared that no competing interests exist.

References

- Fuentes-Pardo A, Brink D, Crean R, Ågren Q, Kultima H, Persson B, Rung J, Lantz H (2025) Presentation of the Swedish Reference Genome Portal at the Living Data 2025 conference - Presentación del Portal Sueco de Genomas de Referencia en la conferencia Datos Vivos 2025. Uppsala University. Presentation. https://doi.org/10.17044/scilifelab.30218329

Endnotes

*1 https://genomes.scilifelab.se/